

11th GERmplasm & Breeding

8th MOLECULAR BIOLOGY

ISSCT WORKSHOP

Saint-Gilles Réunion Island / 1–5 June 2015



« Pushing the frontiers of sugarcane improvement »

ABSTRACT

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SUMMARY

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GENOME WIDE ASSOCIATION MAPPING OF AGRO-MORPHOLOGICAL AND DISEASE RESISTANCE TRAITS IN SUGARCANE

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The objectives of the study were to assess genome wide association study (GWAS) for sugarcane on a panel of 183 accessions and to evaluate the impact of population structure and family relatedness on QTL detection. The panel was genotyped with 3327 AFLP, DArT and SSR markers and phenotyped for 13 traits related to agro-morphology, sugar yield, bagasse content and disease resistances. Marker-trait associations were detected using i/ general linear models (GLM) that took population structure into account with either a Q matrix from STRUCTURE software or principal components (PC) from a principal component analysis added as covariates, and ii/ mixed linear models (MLM) that took into account both population structure and family relatedness estimated using a similarity matrix K* computed using Jaccard's coefficient. With GLM analysis, test statistics were inflated in most cases, while MLM analysis allowed the inflation of test statistics to be controlled in most cases. When only detections in which both population structure and family relatedness were correctly controlled were considered, only 11 markers were significantly associated with three out of the 13. Among these 11 markers, six were linked to the major resistance gene Bru1, which has already been identified. Our results confirm that the use of GWAS is feasible for sugarcane in spite of its complex polyploid genome but also underline the need to take into account family relatedness and not only population structure. The small number of significant associations detected suggests that a larger population and/or denser genotyping are required to increase the statistical power of association detection.

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